

STIC-Biotech/ChemLib

178579

From: Sullivan, Daniel  
Sent: Friday, February 03, 2006 2:42 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search request 09846456

Please search for the following in the issued patent and commercial databases:

An oligo search of SEQ ID-NO: 1, 2, 3 and 5

Thank you.

**Daniel M. Sullivan**

Examiner AU 1636  
Remsen Bldg.  
Room 2A74

Tel: (571) 272-0779

Mailbox: 2C70

RECEIVED  
FEB - 3 2006  
STIC

Oligo search was not done, per our  
phone conversation. To do the regular  
plus oligo searches would add up  
to about 28 hrs, and our limit w/o  
special permission is 20 hours.

If these results are not adequate, we can  
figure out how to proceed. Let me know  
if you require further work.  
Mary Jane Rahl  
Ext. 22524

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model  
Run on: February 8, 2006, 23:04:12 ; Search time 546.227 Seconds  
(without alignments)  
16546.426 Million cell updates/sec

Title: US-09-846-456A-5  
Perfect score: 159  
Sequence: 1 ttaatgaccacccagggcg.....ctttcagaagagacaaaca 159

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues  
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: gb.env.\*  
4: gb.om.\*  
5: gb.ov.\*  
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7: gb.ph.\*  
8: gb.pr.\*  
9: gb.ro.\*  
10: gb.sts.\*  
11: gb.sv.\*  
12: gb.un.\*  
13: gb.vi.\*  
14: gb.hcg.\*  
15: gb.pi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match %	Length DB ID	Description
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2	159	100.0	357	6 AX351030 Sequence
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5	155.8	98.0	10442	6 CS108251 Sequence
6	155.8	98.0	10442	6 AR607250 Sequence
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8	155.8	98.0	10442	6 AX060713 Sequence
9	155.8	98.0	10442	6 AX060892 Sequence
10	155.8	98.0	10442	8 AF285167 Homo sapi
11	155.8	98.0	10474	6 AR607255 Sequence
12	155.8	98.0	10474	6 AR607256 Sequence
13	155.8	98.0	10474	6 AR628830 Sequence
14	155.8	98.0	10474	6 AR628831 Sequence
15	155.8	98.0	10474	6 AX060719 Sequence
16	155.8	98.0	10474	6 AX060721 Sequence
17	155.8	98.0	10474	6 AX060898 Sequence
18	155.8	98.0	10474	6 AX060900 Sequence

19	155.8	98.0	149034	8	AF275948	Homo sapi
20	153.2	96.4	183999	6	AX092589	Sequence
21	143.4	90.2	697	8	AF258627	Homo sapi
22	142.2	89.4	200	8	AF258624	Homo sapi
23	142.2	89.4	446	6	AX127764	Sequence
24	142.2	89.4	446	6	AX127764	Sequence
25	142.2	89.4	447	6	BD117945	EST and e
26	142.2	89.4	447	6	AR422392	Sequence
27	142.2	89.4	447	6	AX983086	Sequence
28	142.2	89.4	480	8	HS252277	Homo sapi
29	142.2	89.4	1062	6	AR583753	Sequence
30	142.2	89.4	1062	6	AX616417	Sequence
31	142.2	89.4	7260	6	AX253452	Sequence
32	142.2	89.4	9741	6	AX127830	Sequence
33	142.2	89.4	9741	6	AX139817	Sequence
34	142.2	89.4	9741	6	AX351038	Sequence
35	142.2	89.4	9854	6	AX127831	Sequence
36	142.2	89.4	9854	6	AX139818	Sequence
37	142.2	89.4	10412	6	CQ785966	Sequence
38	142.2	89.4	10412	6	CQ981355	Sequence
39	142.2	89.4	10412	6	CS031387	Sequence
40	142.2	89.4	10412	6	CS036636	Sequence
41	142.2	89.4	10412	6	CS040339	Sequence
42	142.2	89.4	10412	6	CS045588	Sequence
43	142.2	89.4	10545	6	AR393492	Sequence
44	142.2	89.4	129608	8	AL353685	Human DNA
45	142.2	89.4	175064	14	AC012230	Homo sapi

ALIGNMENTS

RESULT 1  
AX351033  
LOCUS AX351033 159 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 5 from Patent WO0183746.  
ACCESSION AX351033  
VERSION AX351033.1 GI:18616389  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Rosier-Montus, M.F., Prades, C., Lemoine C., Naudin, L., Denefle, P., Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S.  
TITLE Regulatory nucleic acid sequences of the abci gene  
JOURNAL Patent: WO 0183746-A 5 08-NOV-2001;  
Aventis Pharma S.A. (FR)  
FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN				
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Best Local Similarity	100.0%	Pred. No. 3.2e-32;		
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Db	1	TTAATGACACGACCGGCGTCCCTGCTGTGTCAGCTCTGGCCGCTGCTTCCAGGCTCCC	60	
Qy	61	GAGCCACACGCTGGCGTGTGGCTGAGGGAACATGGCATTTGGCTCAGTGAAGTTG	120	
Db	61	GAGCCACACGCTGGCGTGTGGCTGAGGGAACATGGCATTTGGCTCAGTGAAGTTG	120	
Qy	121	CTGCTGTGGAAGAACCTCCTTTCAGAGAGAGACAAACA	159	
Db	121	CTGCTGTGGAAGAACCTCCTTTCAGAGAGAGACAAACA	159	

GenCore version 5.1.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 8, 2006, 17:12:15 ; Search time 65.9706 Seconds  
(without alignments)  
16062.998 Million cell updates/sec

Title: US-09-846-456A-5

Perfect score: 159

Sequence: 1 ttaatgaccagccacggcg.....ctttcagaagaacaaca 159

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	159	100.0	357	6	AAD37266 Human ABC
3	159	100.0	357	6	ABL58148 Human ABC
4	157.4	99.0	159	6	ABN99235 Polymorph
5	155.8	98.0	10365	10	ADD94068 Human ATP
6	155.8	98.0	10381	10	ADD94069 Human ATP
7	155.8	98.0	10423	10	ADD94070 Human ATP
8	155.8	98.0	10442	4	Aaf24680 Nucleotid
9	155.8	98.0	10442	4	Aaf24702 Nucleotid
10	155.8	98.0	10442	13	ADP23549 PRO polyp
11	155.8	98.0	10442	14	ADY15089 DNA encod
12	155.8	98.0	10442	14	AEA23717 Human PRO
13	155.8	98.0	10474	4	AAF24685 Nucleotid
14	155.8	98.0	10474	4	AAF24686 Nucleotid
15	155.8	98.0	10474	4	AAF24708 Nucleotid
16	155.8	98.0	10474	4	AAF24707 Nucleotid
17	155.8	98.0	149034	11	ADP65433 Human ABC
18	153.2	96.4	183999	4	AAF92831 Human ABC
19	153.2	96.4	183999	13	ADU76470 Human ABC

20	147	92.5	158	6	ABN99234	Abn99234 Polymorph
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22	143.4	90.2	201	13	ADQ44225	Adq44225 Myocardia
23	143.4	90.2	201	13	ADQ44200	Adq44200 Myocardia
24	143.4	90.2	1402	13	ADQ38534	Adq38534 Human SNP
25	143.4	90.2	1859	13	ADQ38532	Adq38532 Human SNP
26	143.4	90.2	10405	13	ADQ38535	Adq38535 Human SNP
27	142.2	89.4	446	4	AAS04035	Aas04035 Partial h
28	142.2	89.4	1062	8	ACC51110	Acc51110 Human HAB
29	142.2	89.4	7086	4	ABA09200	Aba09200 Human ABC
30	142.2	89.4	7086	4	AAK52667	Aak52667 Human pol
31	142.2	89.4	7260	4	AAI70315	Aai70315 Human ATP
32	142.2	89.4	7260	4	AAD21326	Aad21326 Human ATP
33	142.2	89.4	7281	4	AAK51683	Aak51683 Human pol
34	142.2	89.4	9741	4	AAS06120	Aas06120 Human ABC
35	142.2	89.4	9741	6	ABL58146	AbL58146 Human ABC
36	142.2	89.4	9854	4	AAS06121	Aas06121 Human ABC
37	142.2	89.4	9870	6	ABN99307	Abn99307 Polymorph
38	142.2	89.4	9870	6	ABN99302	Abn99302 Polymorph
39	142.2	89.4	9870	6	ABN99305	Abn99305 Polymorph
40	142.2	89.4	9870	6	ABN99317	Abn99317 Polymorph
41	142.2	89.4	9870	6	ABN99321	Abn99321 Polymorph
42	142.2	89.4	9870	6	ABN99323	Abn99323 Polymorph
43	142.2	89.4	9870	6	ABN99309	Abn99309 Polymorph
44	142.2	89.4	9870	6	ABN99329	Abn99329 Polymorph
45	142.2	89.4	9870	6	ABN99329	Abn99329 Polymorph

## ALIGNMENTS

### RESULT 1

AAD37269

ID AAD37269 standard; DNA; 159 BP.

XX

AC AAD37269;

XX 21-AUG-2002 (first entry)

XX Human ABC1 gene exon 1B DNA.

XX Human; ATP-binding cassette 1; ABC1 gene regulation; atherosclerosis;  
KW cholesterol metabolism; hypercholesterolaemia; antisense therapy;  
KW exon 1B; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 94..159

FT /\*tag= a

FT /product= "Protein encoded by human ABC1 gene exon 1B"

FT /note= "CDS does not include stop codon"

FT /partial

XX WO200183746-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-EP005488.

XX 02-MAY-2000; 2000US-0201280P.

XX (AVET ) AVENTIS PHARMA SA.

XX Rosier-Montus M, Prades C, Lemoine C, Naudin L, Deneffe P;

XX Brewer B, Duverger N, Remaley A, Santamarina-Fejo S;

XX WPI; 2002-154404/20.

XX P-PSDB; AAE22999.

XX Isolated nucleic acid useful for modifying the ATP-binding cassette 1  
(ABC1) and screening for candidate modulatory compounds or substances.

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OM nucleic - nucleic search, using sw model

Run on: February 9, 2006, 15:01:42 ; Search time 444.338 Seconds  
(without alignments)  
16742.090 Million cell updates/sec

Title: US-09-846-456A-5  
Perfect score: 159  
Sequence: 1 ttaataaccagccacggcg.....ctttcagaagaacaaaca 159

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: gb\_est6.\*  
7: gb\_est7.\*  
8: gb\_est8.\*  
9: gb\_gss1.\*  
10: gb\_gss2.\*  
11: gb\_gss3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155.8	98.0	547	1	AL698654 DKFP686N12109
2	155.8	98.0	583	3	BP280727 BP280727
3	155.8	98.0	595	3	BP280045 BP280045
4	142.2	89.4	583	3	BP200657 BP200657
5	142.2	89.4	583	3	BP287529 BP287529
6	142.2	89.4	663	5	BX955241 DKFP781F
7	140.6	88.4	736	1	AU135588 AU135588
8	105.4	66.3	648	9	B2865821 CH240 259
9	72.8	45.8	619	2	B657864 B657864
10	72.8	45.8	4783	4	AK051920 Mus muscu
11	70.8	44.5	292	8	Z44377 HSC12B081 n
12	70.8	44.5	535	2	BG384217 303216 MA
13	54	34.0	490	8	DN853427 4149571 B
14	44.8	28.2	668	8	CX260141 1313535 N
15	44.8	28.2	742	5	BX911478 BX911478
16	44	27.7	862	7	CO927141 AGENCOURT
17	43.4	27.3	641	3	BJ901916 BJ901916
18	42.6	26.8	1284	4	CR645863 Tetraodon
19	40	25.2	340	5	BY175500 BY175500
20	39.8	25.0	696	7	CO358299 DR ATE OR
21	38.4	24.2	605	1	AJ732100 AJ732100
22	38.4	24.2	687	1	AJ732095 AJ732095

C	23	37	23.3	440	1	AA914462
	24	36.6	23.0	640	5	BW197209 BW197209
	25	36.4	22.9	250	5	BY197692 BY197692
	26	36	22.6	520	1	AV955395 AV955395
C	27	36	22.6	533	1	AV845237 AV845237
	28	36	22.6	587	5	BW325075 BW325075
	29	36	22.6	623	5	BW343397 BW343397
	30	36	22.6	651	5	BW035269 BW035269
	31	36	22.6	685	5	BW251404 BW251404
	32	35.6	22.4	514	9	BH087817 RCIC-24-3
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C	36	35	22.0	963	5	BQ944075 AGENCOURT
	37	34.8	21.9	301	1	AW751638 RCS-CT007
	38	34.8	21.9	343	5	BY197460 BY197460
	39	34.8	21.9	350	5	BY196960 BY196960
	40	34.8	21.9	358	5	BY177088 BY177088
	41	34.8	21.9	358	5	BY210952 BY210952
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## ALIGNMENTS

RESULT 1  
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LOCUS DKFP686N12109\_r1 686 (synonym: hicc3) Homo sapiens CDNA clone  
DEFINITION DKFP686N12109 5', mRNA sequence.  
ACCESSION AL698654  
VERSION AL698654.1 GI:19619194  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 547)  
AUTHORS Dueterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and  
Wiemann, S.  
TITLE EST (Dueterhoeft, et al.)  
JOURNAL Unpublished (1999)  
COMMENT Contact: MIPS  
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by Olagen (Hilden/Germany) within the CDNA sequencing  
consortium of the German Genome Project.  
No sl sequence available.  
This clone (DKFP686N12109) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.  
Location/Qualifiers  
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Best Local Similarity 98.7%; Pred. No. 3.1e-33;

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 19:02:01 ; Search time 90.4911 Seconds  
(without alignments)  
14529.947 Million cell updates/sec

Title: US-09-846-456A-5

Perfect score: 159  
Sequence: 1 ttaatgaccagccacggcg.....ctttcagaagaagacaaaca 159

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	159	100.0	159	3	US-09-846-456-5
2	159	100.0	357	3	US-09-846-456-2
3	159	100.0	357	3	US-09-846-827-4
4	157.4	99.0	159	3	US-09-984-827-26
5	155.8	98.0	10365	5	US-10-098-939-1
6	155.8	98.0	10381	5	US-10-098-939-2
7	155.8	98.0	10423	5	US-10-098-939-3
8	155.8	98.0	10442	8	US-10-972-836-1
9	155.8	98.0	10442	9	US-10-972-836-1
10	155.8	98.0	10474	8	US-10-920-989-7
11	155.8	98.0	10474	8	US-10-920-989-9
12	155.8	98.0	10474	9	US-10-972-836-7
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14	155.8	98.0	149034	9	US-10-287-436A-956
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16	153.2	96.4	183999	8	US-10-872-113-1
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22	143.4	90.2	201	8	US-10-741-600-5805
23	143.4	90.2	201	8	US-10-741-600-5863

## ALIGNMENTS

## RESULT 1

US-09-846-456-5  
; Sequence 5, Application US/09846456

; Patent No. US20020146792A1

; GENERAL INFORMATION:

; APPLICANT: Rosier, Marie

; APPLICANT: Prades, Catherine

; APPLICANT: Lemoine, Cendrine

; APPLICANT: Naudin, Laurent

; APPLICANT: Deneffe, Patrice

; APPLICANT: Duverger, Nicolas

; APPLICANT: Brewer, Bryan

; APPLICANT: Remaley, Alan

; APPLICANT: Fofo, Silvia

; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying

; TITLE OF INVENTION: Activity and Therapeutic Uses

; FILE REFERENCE: 3806.0505

; CURRENT APPLICATION NUMBER: US/09/846.456

; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: US 60/201,280

; PRIOR FILING DATE: 2000-05-02

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5

; LENGTH: 159

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-846-456-5

Query Match

Best Local Similarity 100.0%; Score 159; DB 3; Length 159;

Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAATGACCAAGCCACCGGGCGTCCCTGTGTGTCAGCTTGGCGCGTCTTCCAGGGCTCCC 60

Db 1 TTAATGACCAAGCCACCGGGCGTCCCTGTGTGTCAGCTTGGCGCGTCTTCCAGGGCTCCC 60

Qy 61 GAGCCACACCTGGCGGTGCTGGCTGAGGAACATGCGATGTTGGCTCAGCTGAGGTTG 120

Db 61 GAGCCACACCTGGCGGTGCTGGCTGAGGAACATGCGATGTTGGCTCAGCTGAGGTTG 120

Qy 121 CTGCTGTGGGAAGAACCTTCACTTTTCAGAGAAGACAAACA 159

Db 121 CTGCTGTGGGAAGAACCTTCACTTTTCAGAGAAGACAAACA 159

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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 22:47:42 ; Search time 42.2643 Seconds  
(without alignments)  
3382.690 Million cell updates/sec

Title: US-09-846-456A-5  
Perfect score: 159  
Sequence: 1 ttaatgaccacccggcg.....ctttcagaagaagacaaaca 159

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6240305 seqs, 449581930 residues

Total number of hits satisfying chosen parameters: 12480610

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:  
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4: /cgn2\_6/ptodata/1/pubpna/ECT\_NEW\_PUB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	143.4	90.2	201	7	US-10-995-561-3388
2	143.4	90.2	201	7	US-10-995-561-3388
3	143.4	90.2	201	7	US-10-995-561-3411
4	143.4	90.2	201	7	US-10-995-561-3429
5	143.4	90.2	201	7	US-10-995-561-23954
6	143.4	90.2	1402	7	US-10-995-561-85
7	143.4	90.2	1859	7	US-10-995-561-84
8	143.4	90.2	10405	7	US-10-995-561-83
9	142.2	89.4	159138	7	US-10-995-561-13230
10	64.4	40.5	6786	11	US-11-055-309A-7
11	57	35.8	201	7	US-10-995-561-24507
12	34.6	21.8	6768	11	US-11-043-889-1
13	34.6	21.8	168516	11	US-11-121-086-3
14	33.2	20.9	6432	11	US-11-043-889-3
15	31.2	19.6	5571	7	US-10-750-185-53588
16	31.2	19.6	5571	7	US-10-750-623-53588
17	31.2	19.6	15057	11	US-11-124-367A-5010
18	31.2	19.6	16139	11	US-11-124-367A-5015
19	30.4	19.1	155515	11	US-11-112-908-42
20	30.4	19.1	159660	11	US-11-112-908-43
21	30.4	19.1	177623	11	US-11-112-908-41

c	22	29.6	18.6	1178	11	US-11-112-908-479	Sequence 479, App
	23	29	18.2	34554	6	US-10-893-483-49	Sequence 49, Appl
	24	28.8	18.1	3903	11	US-11-177-000-1	Sequence 1, Appl
c	25	28.2	17.7	600	7	US-10-750-185-21614	Sequence 21614, A
	26	28.2	17.7	600	7	US-10-750-623-21614	Sequence 21614, A
c	27	28.2	17.7	1467	7	US-10-750-185-60794	Sequence 60794, A
	28	28.2	17.7	1467	7	US-10-750-623-60794	Sequence 60794, A
c	29	28.2	17.7	611587	11	US-11-117-187-209	Sequence 209, App
	30	28	17.6	471	11	US-11-112-908-426	Sequence 426, App
c	31	28	17.6	2038	11	US-11-000-463-601	Sequence 601, App
	32	28	17.6	2412	11	US-11-000-463-129	Sequence 129, App
c	33	28	17.6	40000	7	US-10-995-561-13509	Sequence 13509, A
	34	28	17.6	100000	11	US-11-124-368A-2899	Sequence 2899, Ap
c	35	28	17.6	149419	11	US-11-112-908-49	Sequence 49, Appl
	36	28	17.6	161726	11	US-11-112-908-48	Sequence 48, Appl
c	37	28	17.6	161726	11	US-11-112-908-52	Sequence 52, Appl
	38	28	17.6	161726	11	US-11-112-908-47	Sequence 47, Appl
c	39	28	17.6	161726	11	US-11-112-908-41	Sequence 41, Appl
	40	27.8	17.5	67467	11	US-11-124-368A-2889	Sequence 2889, Ap
c	41	27.8	17.5	150038	11	US-11-121-086-23	Sequence 23, Appl
	42	27.4	17.2	201	7	US-10-995-561-49253	Sequence 49253, A
c	43	27.4	17.2	201	7	US-10-995-561-49333	Sequence 49333, A
	44	27.4	17.2	201	11	US-11-124-368A-13339	Sequence 13339, A
c	45	27.4	17.2	201	11	US-11-124-368A-13502	Sequence 13502, A

ALIGNMENTS

RESULT 1  
US-10-995-561-3388  
; Sequence 3388, Application US/109955561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3388  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-995-561-3388

Query Match	90.2%	Score 143.4	DB 7	Length 201
Best Local Similarity	97.5%	Pred. No. 3.5e-33		
Matches 155	Conservative 1	Mismatches 2	Indels 1	Gaps 1
Qy	1	TTAATGACACGACCGGCGCTCCCTGCTGTCAGCTCTGGCGCTCCCTTCAGGGCTCCC	60	
Db	27	TTAATGACACGACCGAC-GGCGCTCCCTGCTGTCAGCTCTGGCGCTCCCTTCAGGGCTCCC	85	
Qy	61	GAGCCACACGCTGGCGCTGCTGGCTGAGGAAACATGGCATGTTGGCTTCAGCTGAGGTG	120	
Db	86	GAGCCACACGCTGGCGGTGCTGGCTGAGGAAACATGGCATGTTGGCTTCAGCTGAGGTG	145	
Qy	121	CTGC	159	
Db	146	CTGC	184	

RESULT 2  
US-10-995-561-3411  
; Sequence 3411, A  
; Publication No. 1  
; GENERAL INFORMATION:  
; APPLICANT: CARG  
; TITLE OF INVENT

TED WITH

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2006, 23:04:12 ; Search time 938.59 Seconds  
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16546.426 Million cell updates/sec

Title: US-09-846-456A-3

Perfect score: 2893

Sequence: 1 acaggcatgtggcaggtg.....ctagtcggcgaaccccc 2893

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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12: gb\_pi.\*

13: gb\_pi.\*

14: gb\_pi.\*

15: gb\_pi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2893	100.0	2893	6	AX351031	Sequence
2	2893	100.0	2231	6	AX351029	Sequence
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C 4	2783.6	96.2	96717	8	AL359182	Human DNA
5	2618.8	90.5	201144	8	AF287262	Homo sapi
C 6	1973.6	68.2	183930	14	AC160520	Papio ham
7	1878	64.9	200920	14	AC161030	Colobus g
8	1435	49.6	149034	8	AF275948	Homo sapi
9	1394.4	48.2	1643	6	AF607251	Sequence
10	1394.4	48.2	1643	6	AR628826	Sequence
11	1394.4	48.2	1643	6	AR607015	Sequence
12	1394.4	48.2	1643	6	AR606894	Sequence
C 13	1393.8	48.2	183118	14	AC160722	Aotus nan
C 14	1332.4	46.1	206547	14	AC161097	Callitru
15	1317.6	45.5	198224	14	AC161090	Callitru
16	1027.8	35.5	1197	6	AR575615	Sequence
17	1010.4	34.9	248297	14	AC160525	Saimiri b
18	889.8	30.8	175064	14	AC012230	Homo sapi

19	889.4	30.7	1167	8	AF258623	Homo sapi
20	889.4	30.7	1167	8	HA252201	Homo sapi
21	612.2	21.2	900	6	CQ769943	Sequence
22	612.2	21.2	900	6	CQ769944	Sequence
23	612.2	21.2	900	6	CQ786993	Sequence
24	612.2	21.2	900	6	CQ786994	Sequence
C 25	553.8	19.1	175064	14	AC012230	Homo sapi
26	478.8	16.5	90698	14	AC021345	Homo sapi
27	414	14.3	69570	14	AC021246	Homo sapi
C 28	377.6	13.1	166049	8	AC090947	Homo sapi
C 29	377.6	13.1	185608	8	AC027126	Homo sapi
C 30	377	13.0	164888	14	AC024101	Homo sapi
C 31	356.4	12.3	162268	8	AC146385	Pan trogl
C 32	356	12.3	81117	8	AC016898	Homo sapi
33	353.8	12.2	175999	14	AC021154	Homo sapi
34	352.2	12.2	167787	8	AC010624	Homo sapi
C 35	351.6	12.2	166743	8	AP003357	Homo sapi
36	351.6	12.2	181953	14	AC087826	Homo sapi
C 37	350.4	12.1	99593	8	HSJ857M17	Human DNA
C 38	349.4	12.1	184640	8	AC009690	Homo sapi
C 39	349.2	12.1	163218	8	AC005837	Homo sapi
40	348	12.0	206231	8	AL592309	Human DNA
C 41	347.8	12.0	159110	8	AL355296	Human DNA
C 42	347.8	12.0	183960	8	AC013445	Homo sapi
C 43	347.4	12.0	141762	8	HS198C21	Human DNA
C 44	347.2	12.0	173375	14	AC044815	Homo sapi
45	346.8	12.0	53962	8	AC009246	Homo sapi

#### ALIGNMENTS

RESULT 1	AX351031	2893 bp	DNA	linear	PAT 06-FEB-2002
LOCUS	Sequence 3 from Patent WO0183746.				
DEFINITION	AX351031				
ACCESSION	AX351031.1	GI:18616387			
VERSION					
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Deneffe, P., Brewer, B., Duverger, N., Remaley, A. and Santamarina-Fojo, S.				
TITLE	Regulatory nucleic acid sequences of the abcl gene				
JOURNAL	Patent: WO 0183746-A 3 08-NOV-2001;				
FEATURES	Location/Qualifiers				
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	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				

ORIGIN	Query Match	100.0%;	Score 2893;	DB 6;	Length 2893;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 2893;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ACAGGGCATGTCGACGGTCCCTGTATCTCAGTTACTCGGGAGGTGGAGGTGCAATGA	60		
Db	1	ACAGGGCATGTCGACGGTCCCTGTATCTCAGTTACTCGGGAGGTGGAGGTGCAATGA	60		
Qy	61	GCCAGATCGCACCATTGCATCTCCAGCTCGGCAACAAAAGGTGAAACTCCATCTCAATT	120		
Db	61	GCCAGATCGCACCATTGCATCTCCAGCTCGGCAACAAAAGGTGAAACTCCATCTCAATT	120		
Qy	121	AAAAAAAAGAAATGATTTTGGTTCGATTTCAATAGGTAGGAGGAAGGAGGAGG	180		
Db	121	AAAAAAAAGAAATGATTTTGGTTCGATTTCAATAGGTAGGAGGAAGGAGGAGG	180		

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2006, 17:12:15 ; Search time 1200.33 Seconds  
(without alignments)  
16062.998 Million cell updates/sec

Title: US-09-846-456A-3

Perfect score: 2893

Sequence: 1 acaggcgtatggtgagtg.....ctagtcggcgaatacccc 2893

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 993994

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Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2893	100.0	2893	6	ABN99232 Human ABC
2	2893	100.0	2910	6	AAD37267 Human ABC
3	2893	100.0	3231	6	AAD37265 Human ABC
4	2893	100.0	3231	6	ABL58147 Human ABC
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6	2891.4	99.9	2893	6	ABN99342 Polymorph
7	2891.4	99.9	2893	6	ABN99354 Polymorph
8	2891.4	99.9	2893	6	ABN99340 Polymorph
9	2891.4	99.9	2893	6	ABN99345 Polymorph
10	2891.4	99.9	2893	6	ABN99347 Polymorph
11	2891.4	99.9	2893	6	ABN99336 Polymorph
12	2891.4	99.9	2893	6	ABN99339 Polymorph
13	2891.4	99.9	2893	6	ABN99352 Polymorph
14	2891.4	99.9	2893	6	ABN99341 Polymorph
15	2891.4	99.9	2893	6	ABN99348 Polymorph
16	2891.4	99.9	2893	6	ABN99357 Polymorph
17	2891.4	99.9	2893	6	ABN99344 Polymorph
18	2891.4	99.9	2893	6	ABN99351 Polymorph
19	2891.4	99.9	2893	6	ABN99353 Polymorph

20	2891.4	99.9	2893	6	ABN99343	Abn99343 Polymorph	
21	2881	99.6	2895	6	ABN99346	Abn99346 Polymorph	
22	2875	99.4	2889	6	ABN99349	Abn99349 Polymorph	
23	2873	99.3	2888	6	ABN99355	Abn99355 Polymorph	
24	2873	99.3	2903	6	ABN99337	Abn99337 Polymorph	
25	2865	99.0	2884	6	ABN99350	Abn99350 Polymorph	
26	2790.2	96.4	183999	4	AAF92831	Aaf92831 Human ABC	
27	2790.2	96.4	183999	13	ADU76470	Adu76470 Human ABC	
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	32	1394.4	48.2	1643	4	AAF24703	Aaf24703 Nucleotid
	33	1027.8	35.5	1197	6	ABL58400	AbL58400 Human lar
	34	899.4	30.7	1033	8	ACC49024	Acc49024 ABC1 gene
	35	857.8	29.7	1115	8	ACC49021	Acc49021 ABC1 gene
	36	612.2	21.2	900	12	ADJ77896	Adj77896 Phenotype
	37	612.2	21.2	900	12	ADJ77895	Adj77895 Phenotype
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	39	350.4	12.1	79544	12	ADQ97764	Adq97764 Human can
	40	336.4	11.6	151909	14	ABE96535	Aeb96535 Human CAB
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	42	330.8	11.4	20645	4	AAI05355	Aal05355 Human rep
	43	330.8	11.4	20645	4	ABL98224	AbL98224 Human tes
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#### ALIGNMENTS

RESULT 1

ABN99232

ID ABN99232 standard; DNA; 2893 BP.

XX AC ABN99232;

XX DT 17-JAN-2003 (first entry)

XX DE Human ABCA1 transporter gene promoter.

XX KW Human; ABCA1; transporter; ATP-binding cassette;

XX KW high density lipoprotein; HDL; cholesterol; familial HDL deficiency;

XX KW Tangier disease; myocardial infarction; atherosclerosis;

XX KW cardiovascular disease; promoter; ds.

XX OS Homo sapiens.

XX PN WO200236770-A2.

XX PD 10-MAY-2002.

XX PF 12-OCT-2001; 2001WO-FR003182.

XX PR 31-OCT-2000; 2000FR-00014037.

XX PA 11-DEC-2000; 2000US-0254108P.

XX PA (AVET ) AVENTIS PHARMA SA.

XX PI (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.

XX PI Denefle P, Rosier M, Arnould-Reguigne I, Duverger N, Cambien F;

XX DR WPI; 2002-435691/46.

XX PT New polymorphisms in the human ABCA1 gene, useful for diagnosing predisposition to myocardial infarct and other cardiovascular diseases.

XX PS Claim 4; Page 109; 297pp; French.

XX CC The present sequence is the human ATP-binding cassette (ABCA1)

XX CC transporter gene promoter. This sequence can be used for diagnosing

XX CC (predisposition to) diseases associated with the plasma level of high

XX CC density lipoprotein (HDL) cholesterol, especially familial HDL deficiency



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OM nucleic - nucleic search, using sw model  
Run on: February 9, 2006, 15:01:42 ; Search time 8084.71 Seconds  
(without alignments)  
16742.090 Million cell updates/sec

Title: US-09-846-456A-3  
Perfect score: 2893  
Sequence: 1 acagggcatggtggcagggtg.....ctagtcgccggaacacccc 2893

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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- 5: gb\_est5.\*
- 6: gb\_est6.\*
- 7: gb\_est7.\*
- 8: gb\_est8.\*
- 9: gb\_est9.\*
- 10: gb\_est10.\*
- 11: gb\_est11.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 4	275.6	9.5	4503	CR858665	Pongo pyg
C 5	267	9.2	1122	AY927481	Homo sapi
C 6	247.6	8.6	3127	CR860188	Pongo pyg
C 7	247.2	8.5	3178	AL832411	Homo sapi
C 8	239.6	8.3	4503	CR858665	Pongo pyg
C 9	237.8	8.2	289	AW748338	RC6-BT025
C 10	234.4	8.1	1741	CR603303	full-length
C 11	233	8.1	770	BZ612146	WHACL55TF
C 12	231.2	8.0	1047	AW816516	QVO-ST023
C 13	221.2	7.6	457	BU616112	UI-H-DF0
C 14	220.6	7.6	696	CR936634	Homo sapi
C 15	220.2	7.6	5920	CR936634	Homo sapi
C 16	219.4	7.6	577	AQ265389	CITBI-E1
C 17	218.6	7.6	544	AQ418551	RPCT-11-2
C 18	217.8	7.5	2403	BC035989	Homo sapi
C 19	217	7.5	350	CN268016	170005318
C 20	217	7.5	620	BQ775487	UI-H-FH0
C 21	216.4	7.5	990	BM803650	AGENCOURT
C 22	216.2	7.5	467	BU735183	UI-E-DW0

23	215.4	7.4	897	5	BU52764	AGENCOURT
C 24	215.2	7.4	719	9	AQ475181	CITBI-E1
C 25	215.2	7.4	1686	4	CR619941	full-length
C 26	215.2	7.4	1755	4	CR609780	full-length
C 27	215.2	7.4	2472	4	HSR803556	full-length
C 28	215.2	7.4	5941	4	CR857073	Pongo pyg
C 29	214.8	7.4	477	5	BU660913	cl65f05.2
C 30	214.8	7.4	659	5	BU660648	cl65f05.2
C 31	214.8	7.4	771	5	EX099350	EX099350
C 32	214.8	7.4	782	5	EX348886	EX348886
C 33	214.8	7.4	789	5	EX390419	EX390419
C 34	214.8	7.4	1485	4	CR619058	full-length
C 35	214.8	7.4	1903	4	CR619058	full-length
C 36	214.4	7.4	423	3	BM991096	UI-H-D10
C 37	214.4	7.4	704	11	CR957968	Homo sapi
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C 41	213.4	7.4	666	10	AG075934	Pan trogl
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C 45	213	7.4	514	1	AI754653	cr38c08.x

ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION Pongo pygmaeus mRNA; cDNA DKFZp459M1426 (from clone DKFZp459M1426).  
ACCESSION CR857583  
VERSION CR857583.1 GI:55726174  
KEYWORDS HNC.  
SOURCE Pongo pygmaeus (orangutan)  
ORGANISM Pongo pygmaeus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Pongo.

REFERENCE 1 (bases 1 to 3004)  
AUTHORS Koehrer, K., Beyer, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.  
CONSTRM The German cDNA Consortium  
TITLE Direct Submission  
JOURNAL Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY  
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by BWPZ (Biomedical Research Center at the Heinrich-Heine-University, Duesseeldorf/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp459M1426) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:  
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp459M1426  
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.

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/note="WD-repeat protein 12 (Homo sapiens)"  
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/gene="DKFZp459M1426"  
166..1437  
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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 19:02:01 ; Search time 1646.48 Seconds  
(without alignments)  
14529.947 Million cell updates/sec

Title: US-09-846-456A-3

Perfect score: 2893

Sequence: 1 acaggcagtggtgagcagtg.....ctagtcggcggcaaaacccc 2893

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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3	2893	100.0	3231	3	US-09-846-456-1	Sequence 1, Appli
4	2893	100.0	3231	3	US-09-846-456-1	Sequence 3, Appli
5	2891.4	99.9	2893	3	US-09-846-827-137	Sequence 137, App
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15	2891.4	99.9	2893	3	US-09-846-827-149	Sequence 149, App
16	2891.4	99.9	2893	3	US-09-846-827-152	Sequence 152, App
17	2891.4	99.9	2893	3	US-09-846-827-153	Sequence 153, App
18	2891.4	99.9	2893	3	US-09-846-827-154	Sequence 154, App
19	2891.4	99.9	2893	3	US-09-846-827-155	Sequence 155, App
20	2891.4	99.9	2893	3	US-09-846-827-157	Sequence 157, App
21	2891.4	99.9	2893	3	US-09-846-827-158	Sequence 158, App
22	2881	99.6	2895	3	US-09-846-827-147	Sequence 147, App
23	2875	99.4	2889	3	US-09-846-827-150	Sequence 150, App

Sequence 156, App  
Sequence 138, App  
Sequence 151, App  
Sequence 6777, App  
Sequence 17613, A  
Sequence 1, Appli  
Sequence 956, App  
Sequence 3, Appli  
Sequence 3, Appli  
Sequence 46, Appli  
Sequence 8043, Ap  
Sequence 17651, A  
Sequence 675, App  
Sequence 12, Appli  
Sequence 85, Appli  
Sequence 85, Appli  
Sequence 104, App  
Sequence 17708, A  
Sequence 17735, A  
Sequence 718, App

## ALIGNMENTS

## RESULT 1

US-09-846-456-3

; Sequence 3, Application US/09846456

; Patent No. US20020146792A1

; GENERAL INFORMATION:

; APPLICANT: Rosier, Marie

; APPLICANT: Prades, Catherine

; APPLICANT: Lemoine, Cendrline

; APPLICANT: Naudin, Laurence

; APPLICANT: Deneffe, Patrice

; APPLICANT: Duverger, Nicolas

; APPLICANT: Brewer, Bryan

; APPLICANT: Remaley, Alan

; APPLICANT: Pojo, Silvia

; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying

; TITLE OF INVENTION: Activity and Therapeutic Uses

; FILE REFERENCE: 3806.0505

; CURRENT APPLICATION NUMBER: US/09/846.456

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: US 60/201,280

; PRIOR FILING DATE: 2000-05-02

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 2893

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-846-456-3

Query Match 100.0%; Score 2893; DB 3; Length 2893;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2893; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 61 GCCCAGATCGCACCAATTCGCTCAGCTGGGCAACAAAGGTGAACTCCATCTCAATT 120  
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Qy 181 AGATGGAGGGTTCAGGAGATCTAATTAATCTCTTAAATATCATGCTAGGAAGATAACACCT 240



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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 19:02:01 ; Search time 203.178 Seconds  
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14529.947 Million cell updates/sec

Title: US-09-846-456A-2  
Perfect score: 357  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	340.2	95.3	10545	7	US-10-617-334-14
10	340.2	95.3	10545	7	US-10-744-465-14
11	340.2	95.3	10545	8	US-10-833-679-14
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18	203.8	57.1	1062	5	US-10-000-986-101
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20	203.8	57.1	1062	6	US-10-001-142-101
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24	159.4	44.6	10442	8	US-10-920-989-1	Sequence 1, Appli
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27	159.4	44.6	10474	8	US-10-920-989-9	Sequence 9, Appli
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33	159.4	44.6	10474	9	US-10-972-836-9	Sequence 9, Appli
34	159.4	44.6	10474	9	US-10-972-836-9	Sequence 9, Appli
35	159.4	44.6	10474	9	US-10-972-836-9	Sequence 9, Appli
36	159.4	44.6	10474	9	US-10-972-836-9	Sequence 9, Appli
37	159.4	44.6	10474	9	US-10-972-836-9	Sequence 9, Appli
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ALIGNMENTS

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; Sequence 2, Application US/09846456  
; Patent No. US20020146792A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosier, Marie  
; APPLICANT: Prades, Catherine  
; APPLICANT: Lemoine, Cendrine  
; APPLICANT: Naudin, Laurent  
; APPLICANT: Benfle, Patrice  
; APPLICANT: Duverger, Nicolas  
; APPLICANT: Brewer, Bryan  
; APPLICANT: Remaley, Alan  
; APPLICANT: Pojo, Silvia  
; TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modifying  
; FILE REFERENCE: 3806.0505  
; CURRENT APPLICATION NUMBER: US/09/846,456  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/201,280  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 357  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-846-456-2  
Query Match 100.0%; Score 357; DB 3; Length 357;  
Best Local Similarity 100.0%; Pred. No. 3.9e-105; Indels 0; Gaps 0;  
Matches 357; Conservative 0; Mismatches 0;  
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GenCore version 5.1.7  
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16062.998 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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14: geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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7	203.8	57.1	1062	8	ACC51110 Human ABC
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9	159.4	44.6	10442	4	AAF24702 Nucleotid
10	159.4	44.6	10442	13	ADP23549 PRO polyp
11	159.4	44.6	10442	14	ADY15089 DNA encod
12	159.4	44.6	10442	14	AEA23717 Human PRO
13	159.4	44.6	10474	4	AAF24685 Nucleotid
14	159.4	44.6	10474	4	AAF24686 Nucleotid
15	159.4	44.6	10474	4	AAF24708 Nucleotid
16	159.4	44.6	10474	4	AAF24707 Nucleotid
17	159	44.5	159	6	AAD37269 Human ABC
18	158.4	44.4	10381	10	ADD94069 Human ATP
19	158.4	44.4	10423	10	ADD94070 Human ATP

20	157.4	44.1	159	6	ABN99235
21	157.4	44.1	10385	10	ADD94068
22	147	41.2	158	6	ABN99234
23	147	41.2	1402	13	ADQ38534
24	147	41.2	1859	13	ADQ38532
25	147	41.2	10405	13	ADQ38535
26	146.4	41.0	201	13	ADQ44142
27	146.4	41.0	201	13	ADQ44225
28	146.4	41.0	201	13	ADQ44200
29	145.8	40.8	446	4	AAS04035
30	145.8	40.8	7086	4	ABA09200
31	145.8	40.8	7086	4	AAK52667
32	145.8	40.8	7260	4	AAI70315
33	145.8	40.8	7260	4	AAD21326
34	145.8	40.8	7281	4	AAK51683
35	145.8	40.8	9741	4	AAS06120
36	145.8	40.8	9741	6	ABL37273
37	145.8	40.8	9741	6	ABL58146
38	145.8	40.8	9854	4	AAS06121
39	145.8	40.8	9870	6	ABN99307
40	145.8	40.8	9870	6	ABN99302
41	145.8	40.8	9870	6	ABN99305
42	145.8	40.8	9870	6	ABN99317
43	145.8	40.8	9870	6	ABN99321
44	145.8	40.8	9870	6	ABN99323
45	145.8	40.8	9870	6	ABN99309

## ALIGNMENTS

## RESULT 1

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ID AAD37266 standard; DNA; 357 BP.

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AC AAD37266;

XX  
DT 21-AUG-2002 (first entry)

XX  
DE Human ABC1 transcription regulatory DNA #2.

XX  
KW Human; ATP-binding cassette 1; ABC1 gene regulation; atherosclerosis; cholesterol metabolism; hypercholesterolaemia; antisense therapy; ds.

XX  
OS Homo sapiens.

XX  
FN WO200183746-A2.

XX  
PD 08-NOV-2001.

XX  
PF 02-MAY-2001; 2001WO-EP005488.

XX  
PR 02-MAY-2000; 2000US-0201280P.

XX  
PA (AVET ) AVENTIS PHARMA SA.

XX  
PI Rosier-Montus M, Prades C, Lemoine C, Naudin L, Deneffe P;

XX  
PI Brewer B, Duverger N, Remaley A, Santamarina-Fojo S;

XX  
DR WPI; 2002-154404/20.

XX  
PT Isolated nucleic acid useful for modifying the ATP-binding cassette 1 (ABC1) and screening for candidate modulatory compounds or substances.

XX  
PS Claim 2; Page 131; 152pp; English.

XX  
CC The invention relates a nucleic acid which is capable of regulating the transcription of human ATP-binding cassette 1 (ABC1) gene, which is a casual gene for pathologies linked to a dysfunctioning of cholesterol metabolism, including diseases such as atherosclerosis. Polynucleotides of the invention are used to screen candidate molecules or substances that are capable of modulating the transcription of the ABC1 gene. They are used in antisense therapy. Compositions comprising sequences of the



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OM nucleic - nucleic search, using sw model

Run on: February 8, 2006, 23:04:12 ; Search time 1226.43 Seconds  
(without alignments)  
16546.426 Million cell updates/sec

Title: US-09-846-456A-2

Perfect score: 357

Sequence: 1 tggagggtctcagctgagagg.....gagggaaggaagctgtgttg 357

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb\_ba.\*

2: gb\_in.\*

3: gb\_env.\*

4: gb\_ov.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pt.\*

9: gb\_ro.\*

10: gb\_sts.\*

11: gb\_sy.\*

12: gb\_un.\*

13: gb\_vl.\*

14: gb\_btg.\*

15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	357	100.0	357	6	AX351030	Sequence
2	353.8	99.1	149034	8	AP275948	Homo sapi
3	351.2	98.4	183999	6	AX092589	Sequence
4	340.2	95.3	480	8	HGA252277	Sequence
5	340.2	95.3	10545	6	AR393492	Sequence
6	340.2	95.3	129608	8	AL353685	Human DNA
7	340.2	95.3	175064	14	AC012230	Homo sapi
8	340.2	95.3	201144	8	AP287262	Homo sapi
9	294.2	82.4	183930	14	AC160520	Papio ham
10	294.2	82.4	207933	14	AC160521	Papio ham
11	292.6	82.0	200920	14	AC161030	Colobus g
12	285	79.8	183118	14	AC160722	Aotus nan
13	284	79.6	171939	14	AC160721	Aotus nan
14	280.8	78.7	198224	14	AC161090	Callithri
15	280.8	78.7	208547	14	AC161097	Callicebu
16	271.4	76.0	248297	14	AC160525	Saimiri b
17	251.2	70.4	90698	14	AC021345	Homo sapi
18	231	64.7	179848	14	AC139880	Lemur cat

19	203.8	57.1	1062	6	AR583753	Sequence
20	203.8	57.1	1062	6	AX616417	Sequence
21	203.4	57.0	447	6	BD117945	EST and e
22	203.4	57.0	447	6	AR422392	Sequence
23	203.4	57.0	447	6	AX983086	Sequence
24	184.2	51.6	200	8	AF258623S2	Sequence
25	159.4	44.6	10442	6	CS031389	Sequence
26	159.4	44.6	10442	6	CS040341	Sequence
27	159.4	44.6	10442	6	CS108251	Sequence
28	159.4	44.6	10442	6	AX607250	Sequence
29	159.4	44.6	10442	6	AR628825	Sequence
30	159.4	44.6	10442	6	AX060713	Sequence
31	159.4	44.6	10442	6	AX060892	Sequence
32	159.4	44.6	10442	8	AF285167	Homo sapi
33	159.4	44.6	10474	6	AR607255	Sequence
34	159.4	44.6	10474	6	AR607256	Sequence
35	159.4	44.6	10474	6	AR628830	Sequence
36	159.4	44.6	10474	6	AR628831	Sequence
37	159.4	44.6	10474	6	AX060719	Sequence
38	159.4	44.6	10474	6	AX060721	Sequence
39	159.4	44.6	10474	6	AX060898	Sequence
40	159.4	44.6	10474	6	AX060900	Sequence
41	159	44.5	159	6	AX351033	Sequence
42	147	41.2	697	8	AF258627	Homo sapi
43	145.8	40.8	446	6	AX127764	Sequence
44	145.8	40.8	446	6	AX139751	Sequence
45	145.8	40.8	7260	6	AX253452	Sequence

#### ALIGNMENTS

RESULT 1  
AX351030  
LOCUS AX351030 357 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 2 from Patent WO0183746.  
ACCESSION AX351030  
VERSION AX351030.1 GI:18616386

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Rosier-Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Deneffe, P.,  
Brewer, B., Duverger, N., Remaley, A. and Santamarina-Pojo, S.  
TITLE Regulatory nucleic acid sequences of the abcl gene  
JOURNAL Patent: WO 0183746-A 2 08-NOV-2001;  
Aventis Pharma S.A. (FR)

FEATURES  
source Location/Qualifiers  
1..357  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 100.0%; Score 357; DB 6; Length 357;  
Best Local Similarity 100.0%; Pred. No. 1.8e-94;  
Matches 357; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGAGGTCCTCAGCTGAGAGGCTGGATTAGCAGTCCTCATTTGGTGTATGGCTTTGACGA 60  
DB 1 TGGAGGTCCTCAGCTGAGAGGCTGGATTAGCAGTCCTCATTTGGTGTATGGCTTTGACGA 60

QY 61 ATAACTGATGGCTGTTTCCCTCTCTGCTTATCTTTTCAGTTAATGACACGACGCGGCT 120  
DB 61 ATAACTGATGGCTGTTTCCCTCTCTGCTTATCTTTTCAGTTAATGACACGACGCGGCT 120

QY 121 CCCTGCTGTGAGCTCTGGCGCTCCGCTTCCAGGCTCCGAGCCACACGCTGGGCGTCT 180  
DB 121 CCCTGCTGTGAGCTCTGGCGCTCCGCTTCCAGGCTCCGAGCCACACGCTGGGCGTCT 180

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OM nucleic - nucleic search, using sw model

Run on: February 9, 2006, 15:01:42 : Search time 997.664 Seconds  
(without alignments)  
16742.090 Million cell updates/sec

Title: US-09-846-456A-2

Perfect score: 357

Sequence: 1 tggaggtctcagctgagagg.....gagggaaggaagctgtgttg 357

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb\_est1.\*

2: gb\_est2.\*

3: gb\_est3.\*

4: gb\_est4.\*

5: gb\_est5.\*

6: gb\_est6.\*

7: gb\_est7.\*

8: gb\_est8.\*

9: gb\_est9.\*

10: gb\_est10.\*

11: gb\_est11.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	169.4	47.5	648	9	BZ865821 CH240_259
2	159.4	44.6	547	1	AL698654 DKFZp686N
3	159.4	44.6	583	3	BP280727 BP280727
4	159.4	44.6	595	3	BP280045 BP280045
5	145.8	40.8	583	3	BP200657 BP200657
6	145.8	40.8	663	5	BX555241 DKFZp781P
7	145.2	40.7	583	3	BP287529 BP287529
8	144.2	40.4	736	1	AU135588 AU135588
9	75.8	21.2	619	2	BB657864 BB657864
10	75.8	21.2	4763	4	AK051920 Mus muscu
				8	Z44377 HSC12B081 n
				2	BG384217 303216 MA
				2	DN853427 419571 B
				4	CNS0EXBH
				3	BJ901916 BJ901916
				8	CX260141 1313535 N
				5	BX311478 BX311478
				7	CO227141 AGENCOURT
				5	BY175500 BY175500
				8	DN485045 M102C08.3
				10	CNS02DO1
				5	BU867612 M102C08 P

23	40.8	11.4	442	8	DN494513
24	40.2	11.3	888	6	CB209313
25	39.8	11.1	696	7	CO358299
26	39.6	11.1	910	10	CNS0060N
27	39.4	11.0	562	5	BQ609447
28	39.4	11.0	644	5	BY721914
29	39.4	11.0	659	5	BY728087
30	39.4	11.0	766	6	CB231301
31	39.4	11.0	3468	4	AK081173
32	38.8	10.9	605	1	AK732100
33	38.8	10.9	687	1	AJ732095
34	38.2	10.7	503	1	AV818336
35	38	10.6	1080	5	EX402928
36	37.6	10.5	640	5	BM197209
37	37.4	10.5	878	9	BZ262115
38	37.4	10.5	900	5	BU526370
39	37.4	10.5	926	9	AZ542175
40	37	10.4	4462	1	AA914462
41	37	10.4	520	1	AV955395
42	37	10.4	533	1	AV845237
43	37	10.4	587	5	BM325075
44	37	10.4	623	5	BM343397
45	37	10.4	651	5	BM035269

## ALIGNMENTS

RESULT 1  
BZ865821  
LOCUS  
DEFINITION  
BZ865821 648 bp DNA linear GSS 18-MAR-2003  
CH240\_259B12.TJ CHORI-240 Bos taurus genomic clone CH240\_259B12,  
genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Bos taurus (cow)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.  
REFERENCE  
AUTHORS  
Zhao,S., Shetty,J., Shatsman,S., Teagay,G., Geer,K.,  
Shvartsbeyn,A., Gebregeorgis,E., Chen,D., Riggs,F., de Jong,P.,  
Crawford,A.M. and McEwan,J.C.  
Bovine BAC End Sequences from Library CHORI-240  
Unpublished (2003)  
CONTACT: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm). For BAC library  
availability, please contact Pieter de Jong (pdejong@mail.cho.org).  
Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering\_information.htm). This work  
was undertaken as part of the International Bovine BAC Mapping  
Consortium (IBBMC) by AgResearch Ltd., New Zealand and The  
Institute of Genomic Research (TIGR), USA.

Class: BAC ends.  
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Plate: 259 row: B column: 12  
Location/Qualifiers  
1. 648  
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/clone="CH240\_259B12"  
/sex="Male"





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OM nucleic - nucleic search, using sw model

Run on: February 9, 2006, 15:01:42 ; Search time 9029.28 Seconds  
(without alignments)  
16742.090 Million cell updates/sec

Title: US-09-846-456A-1  
Perfect score: 3231  
Sequence: 1 acaggcatgtgaggtg.....gccccacatccccaccactt 3231

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hic:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gss1:\*  
10: gb\_gss2:\*  
11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	336	10.4	763	1	AU121731	AU121731
C	324	10.0	3004	4	CR857583	Pongo pyg
3	322.2	10.0	3004	4	CR857583	Pongo pyg
4	314.4	9.7	663	5	BX955241	DKFZp781F
5	285.4	8.8	3127	4	CR860188	Pongo pyg
6	275.6	8.5	4503	4	CR858665	Pongo pyg
C	267	8.3	1122	4	AY927481	Homo sapi
C	247.6	7.7	3127	4	CR860188	Pongo pyg
C	247.2	7.7	3178	4	HSM803719	Homo sapi
C	239.6	7.4	4503	4	CR858665	Pongo pyg
C	237.8	7.4	289	1	AW748338	RC6-BT025
C	234.4	7.3	1741	9	CR603303	full-leng
C	233	7.2	770	9	BZ612146	WHACL55TF
C	231.2	7.2	1047	5	BX380958	BP287529
15	223.4	6.9	583	3	BP287529	BP287529
16	221.8	6.9	736	1	AU135588	AU135588
17	221.4	6.9	583	3	BP200657	BP200657
18	221.4	6.9	583	3	BP280727	BP280727
19	221.4	6.9	595	3	BP280045	BP280045
C	220.2	6.8	457	1	AW916516	QV0-ST023
21	220.6	6.8	696	5	BUE16112	UI-H-DFO-
C	220.2	6.8	5920	4	CR936634	Homo sapi

C 23 219.4 6.8 577 9 AQ265389  
24 218.6 6.8 544 9 AQ418551  
25 217.8 6.7 2403 4 BC035989  
26 217 6.7 350 7 CN268016  
27 217 6.7 620 5 BQ775487  
28 216.4 6.7 990 3 BM803650  
29 216.2 6.7 467 5 BU735183  
30 215.4 6.7 897 5 BU552764  
31 215.2 6.7 719 9 AQ475181  
32 215.2 6.7 1686 4 CR619941  
33 215.2 6.7 1755 4 CR609780  
34 215.2 6.7 2472 4 HSM803556  
35 215.2 6.7 5941 4 CR857073  
36 214.8 6.6 477 5 BU660913  
37 214.8 6.6 659 5 BU660648  
38 214.8 6.6 771 5 BX099350  
39 214.8 6.6 782 5 BX348886  
40 214.8 6.6 789 5 BX390419  
41 214.8 6.6 1485 4 CR610354  
42 214.8 6.6 1903 4 CR619058  
43 214.4 6.6 423 3 BM991096  
44 214.4 6.6 704 11 CR957968  
45 214.2 6.6 581 9 AQ347610

## ALIGNMENTS

RESULT 1  
AU121731  
LOCUS AU121731 MAMMAL Homo sapiens cDNA clone MAMMAL000851 5', mRNA linear EST 01-AUG-2002  
DEFINITION AU121731 sequence.  
ACCESSION AU121731  
VERSION AU121731.1 GI:10936966  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 763)  
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.  
HRI human cDNA project  
Unpublished (2000)  
Contact: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: genomics@hri.co.jp  
HRI human cDNA project; 5' & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.  
Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 7e-23;  
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: February 8, 2006, 17:12:15 ; Search time 1340.57 Seconds  
(without alignments)  
16062.998 Million cell updates/sec

Title: US-09-846-456A-1  
Perfect score: 3231  
Sequence: 1 acaggcgatggtgacggtg.....gccccacatcccccaccactt 3231

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq 21:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*
- 14: Geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3231	100.0	3231	6	AAD37265 Human ABC
2	3231	100.0	3231	6	ABL58147 Human ABC
3	3127.8	96.8	183999	4	Aaf92831 Human ABC
4	3127.8	96.8	183999	13	ADU76470 Human ABC
5	3121.6	96.6	21000	13	ADT77194 Type II d
6	2910	90.1	2910	6	AAD37267 Human ABC
7	2893	89.5	2893	6	ABN99332 Human ABC
8	2891.4	89.5	2893	6	ABN99356 Polymorph
9	2891.4	89.5	2893	6	ABN99342 Polymorph
10	2891.4	89.5	2893	6	ABN99354 Polymorph
11	2891.4	89.5	2893	6	ABN99340 Polymorph
12	2891.4	89.5	2893	6	ABN99345 Polymorph
13	2891.4	89.5	2893	6	ABN99347 Polymorph
14	2891.4	89.5	2893	6	ABN99336 Polymorph
15	2891.4	89.5	2893	6	ABN99339 Polymorph
16	2891.4	89.5	2893	6	ABN99352 Polymorph
17	2891.4	89.5	2893	6	ABN99341 Polymorph
18	2891.4	89.5	2893	6	ABN99348 Polymorph
19	2891.4	89.5	2893	6	ABN99357 Polymorph

20	2891.4	89.5	2893	6	ABN99344	Polymorph
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22	2891.4	89.5	2893	6	ABN99353	Polymorph
23	2891.4	89.5	2893	6	ABN99343	Polymorph
24	2881	89.2	2895	6	ABN99346	Polymorph
25	2875	89.0	2889	6	ABN99349	Polymorph
26	2873	88.9	2888	6	ABN99355	Polymorph
27	2873	88.9	2903	6	ABN99337	Polymorph
28	2865	88.7	2884	6	ABN99350	Polymorph
29	2411.4	74.6	2893	6	ABN99338	Polymorph
30	1773	54.9	149034	11	ADP65433	Human ABC
31	1485.4	46.0	1643	4	AAF24681	Nucleotid
32	1485.4	46.0	1643	4	AAF24703	Nucleotid
33	1134.8	35.1	1137	6	ABL58400	Human lar
34	1063.4	32.9	1115	8	ACC49021	ABCI gene
35	996.4	30.8	1033	8	ACC49024	ABCI gene
36	899.2	27.8	900	12	ADJ77896	Phenotype
37	899.2	27.8	900	12	ADJ77895	Phenotype
38	377.6	11.7	166043	12	ADL08127	Human gen
39	350.4	10.8	79544	12	ADQ97764	Human can
40	336.4	10.4	151909	14	ABE96535	Human CAB
41	336	10.4	763	4	AAH04729	Human cDN
42	336	10.4	1750	4	AAH17451	Human cDN
43	333	10.3	80928	12	ADO25290	Human rep
44	330.8	10.2	20645	4	AAI05355	Human tes
45	330.8	10.2	20645	4	ABL98224	Human tes

ALIGNMENTS

RESULT 1  
AAD37265  
ID AAD37265 standard; DNA; 3231 BP.  
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AC AAD37265;  
XX  
XX  
DT 21-AUG-2002 (first entry)  
XX  
DE Human ABC1 transcription regulatory DNA #1.  
XX  
XX Human; ATP-binding cassette 1; ABC1 gene regulation; atherosclerosis;  
KW cholesterol metabolism; hypercholesterolaemia; antisense therapy; ds.  
XX  
OS Homo sapiens.  
XX  
FN WO200183746-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-EP005488.  
XX  
PR 02-MAY-2000; 2000US-0201280P.  
XX  
XX (AVET ) AVENTIS PHARMA SA.  
XX  
PI Rosier-Montus M, Prades C, Lemoine C, Naudin L, Deneffe P;  
PI Brewer B, Duverger N, Remaley A, Santamarina-Pojo S;  
XX  
XX WPI; 2002-154404/20.  
DR  
PT Isolated nucleic acid useful for modifying the ATP-binding cassette 1  
PT (ABC1) and screening for candidate modulatory compounds or substances.  
XX  
PS Claim 1; Page 130-131; 152pp; English.  
XX  
CC The invention relates a nucleic acid which is capable of regulating the  
CC transcription of human ATP-binding cassette 1 (ABC1) gene, which is a  
CC casual gene for pathologies linked to a dysfunctioning of cholesterol  
CC metabolism, including diseases such as atherosclerosis. Polynucleotides  
CC of the invention are used to screen candidate molecules or substances  
CC that are capable of modulating the transcription of the ABC1 gene. They  
CC are used in antisense therapy. Compositions comprising sequences of the





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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 06:52:37 ; Search time 20.1384 Seconds  
(without alignments)  
14034.494 Million cell updates/sec

Title: US-09-846-456A-5

Perfect score: 159

Sequence: 1 ttaatgaccgacccagggcg.....ctttcagaagaagaaca 159

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 898780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
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7: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155.8	98.0	10442	3	US-09-596-141C-1
2	155.8	98.0	10442	3	US-09-595-526C-1
3	155.8	98.0	10474	3	US-09-596-141C-7
4	155.8	98.0	10474	3	US-09-596-141C-9
5	155.8	98.0	10474	3	US-09-595-526C-7
6	155.8	98.0	10474	3	US-09-595-526C-9
7	142.2	89.4	447	3	US-09-621-976-13889
8	142.2	89.4	1062	3	US-10-000-489-101
9	142.2	89.4	10545	3	US-09-526-193A-14
10	135.2	85.0	7860	3	US-09-526-193A-2
11	35.8	22.5	234884	3	US-09-949-016-116420
12	35	22.0	298	3	US-09-513-999C-10257
13	34.6	21.8	8920	3	US-09-949-016-15145
14	34.6	21.8	30678	3	US-09-949-016-12818
15	33.2	20.9	6588	3	US-09-949-016-1076
16	32.8	20.6	137753	3	US-09-949-016-17404
17	32.6	20.5	601	3	US-09-949-016-112405
18	32.6	20.5	601	3	US-09-949-016-112406
19	32.6	20.5	86380	3	US-09-949-016-14837
20	30.6	19.2	2935	3	US-09-976-594-365
21	30.6	19.2	8961	3	US-09-949-016-15910
22	30.4	19.1	390	3	US-09-489-039A-7103
23	30.4	19.1	485	3	US-09-513-999C-1002
24	30.4	19.1	532	3	US-09-513-999C-1003

25 30.4 19.1 2028 3 US-09-949-016-2675 Sequence 2675, Ap  
26 30.4 19.1 36223 3 US-09-949-016-14417 Sequence 14417, A  
27 30.2 19.0 1727 3 US-09-327-983-3 Sequence 3, Appli  
28 30.2 19.0 1727 3 US-09-549-827A-7 Sequence 7, Appli  
29 30.2 19.0 118999 3 US-09-791-1058-32 Sequence 32, Appli  
30 30.2 19.0 118999 3 US-09-735-271-884 Sequence 884, App  
31 30.2 18.9 700 2 US-08-866-650-2 Sequence 2, Appli  
32 30.2 18.9 4771 2 US-09-021-287-2 Sequence 2, Appli  
33 30.2 18.9 4771 3 US-09-240-473-2 Sequence 3, Appli  
34 30.2 18.9 33529 3 US-09-144-085-3 Sequence 17575, A  
35 29.8 18.7 11359 3 US-09-949-016-17575 Sequence 12, Appli  
36 29.8 18.7 118999 3 US-09-791-1058-32 Sequence 1009, Ap  
37 29.6 18.6 425 3 US-09-621-976-1009 Sequence 1219, Ap  
38 29.6 18.6 22761 3 US-09-302-540-1219 Sequence 17202, A  
39 29.4 18.5 364 3 US-09-621-976-17202 Sequence 12849, A  
40 29.4 18.5 373 3 US-09-513-999C-12849 Sequence 7, Appli  
41 29.4 18.5 3147 2 US-08-781-802-7 Sequence 7, Appli  
42 29.4 18.5 3147 3 US-08-694-078-7 Sequence 7, Appli  
43 29.4 18.5 3147 3 US-09-058-260-7 Sequence 7, Appli  
44 29.4 18.5 26640 3 US-09-949-016-17431 Sequence 17431, A  
45 29.2 18.4 14967 3 US-09-949-016-15448 Sequence 15448, A

## ALIGNMENTS

## RESULT 1

US-09-596-141C-1  
; Sequence 1, Application US/09596141C  
; Patent No. 6821774  
; GENERAL INFORMATION:  
; APPLICANT: Lawn, Richard M.  
; APPLICANT: Wade, David  
; APPLICANT: Oram, John F.  
; APPLICANT: Garvin, Michael  
; TITLE OF INVENTION: Compositions and Methods for Increasing Cholesterol Efflux and Raising HDL using APP Binding Cassette  
; TITLE OF INVENTION: Transporter Protein ABC1  
; FILE REFERENCE: 99,395-B  
; CURRENT APPLICATION NUMBER: US/09/596,141C  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: US 60/140,264  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: US 60/153,872  
; PRIOR FILING DATE: 1999-09-14  
; PRIOR APPLICATION NUMBER: US 60/166,573  
; PRIOR FILING DATE: 1999-11-19  
; NUMBER OF SEQ ID NOS: 62  
; SEQ ID NO 1  
; LENGTH: 10442  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(10442)  
; OTHER INFORMATION: All n's are unknown.  
US-09-596-141C-1

Query Match 98.0%; Score 155.8; DB 3; Length 10442;  
Best Local Similarity 98.7%; Pred. No. 8.6e-36;  
Matches 157; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 TTAATGACCAAGCAGCGCGCTCCCTGTGTGTCAGCTCTGGCGCTGCTTCCAGGGCTCCC 60  
Db 198 TTAATGACCAAGCAGCGCGCTCCCTGTGTGTCAGCTCTGGCGCTGCTTCCAGGGCTCCC 257  
Qy 61 GAGCCACACGCTGGGCGTGTGGCTGTAGGGAACATGGCATGTTGGCTCAGCTGAGTTG 120  
Db 258 GAGCCACACGCTGGGCGTGTGGCTGTAGGGAACATGGCATGTTGGCTCAGCTGAGTTG 317  
Qy 121 CTGCTGGGAGAGACCTTACCTTTTCAGAGAGACAAACA 159  
Db 318 CTGCTGGGAGAGACCTTACCTTTTCAGAGAGACAAACA 356

Result No.	Score	Query Match	Length	DB	ID	Description
1	340.2	95.3	10545	3	US-09-526-193A-14	Sequence 14, Appl
2	203.8	57.1	10652	3	US-10-000-489-101	Sequence 101, App
3	203.4	57.0	4447	3	US-09-621-976-13889	Sequence 13889, A
4	159.4	44.6	10442	3	US-09-596-141C-1	Sequence 1, Appl
5	159.4	44.6	10442	3	US-09-595-526C-1	Sequence 1, Appl
6	159.4	44.6	10474	3	US-09-596-141C-7	Sequence 7, Appl
7	159.4	44.6	10474	3	US-09-596-141C-9	Sequence 9, Appl
8	159.4	44.6	10474	3	US-09-595-526C-9	Sequence 9, Appl
9	159.4	44.6	10474	3	US-09-595-526C-9	Sequence 9, Appl
10	135.8	38.0	7860	3	US-09-526-193A-2	Sequence 2, Appl
11	37.8	10.6	8920	3	US-09-949-016-15145	Sequence 15145, A
12	37.8	10.6	30878	3	US-09-949-016-12818	Sequence 12818, A
C 13	36.4	10.2	154600	3	US-09-949-016-14757	Sequence 14757, A
C 14	35.8	10.0	858	3	US-09-540-236-1287	Sequence 1287, Ap
C 15	35.8	10.0	92407	3	US-09-596-002-36	Sequence 36, Appl
C 16	35.8	10.0	234884	3	US-09-949-016-16420	Sequence 16420, A
C 17	35.2	9.9	601	3	US-09-949-016-21645	Sequence 21645, A
C 18	35.2	9.9	601	3	US-09-949-016-156690	Sequence 156690, A
C 19	35.2	9.9	231129	3	US-09-949-016-16110	Sequence 16110, A
C 20	35.2	9.9	266293	3	US-09-949-016-11934	Sequence 11934, A
21	35	9.8	298	3	US-09-513-999C-10257	Sequence 10257, A
22	34.4	9.6	6588	3	US-09-949-016-1076	Sequence 1076, Ap
23	33.4	9.4	4438	3	US-09-949-016-13578	Sequence 13578, A
24	32.8	9.2	137753	3	US-09-949-016-17404	Sequence 17404, A

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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 06:52:37 ; Search time 366,418 Seconds  
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14034,494 Million cell updates/sec

Title: US-09-846-456A-3

Perfect score: 2893

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Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

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- 2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*
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- 8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*
- 9: /cgn2\_6/ptodata/1/ina/backfilesi.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	1394.4	48.2	1643	3	US-09-596-141C-3
2	1394.4	48.2	1643	3	US-09-595-526C-3
3	1027.8	35.5	1197	3	US-09-560-372-1
4	347.4	12.0	118143	3	US-09-949-016-17196
5	335.6	11.6	13821	3	US-09-949-016-13690
6	333	11.5	84870	3	US-09-949-016-17547
7	330.4	11.4	36148	3	US-09-949-016-12969
8	330	11.4	14519	3	US-09-949-016-15611
9	330	11.4	14519	3	US-09-949-016-15612
10	325.2	11.2	31318	3	US-09-949-016-12495
11	325.2	11.2	31319	3	US-09-949-016-15963
12	324.8	11.2	87734	3	US-09-949-016-17521
13	324.4	11.2	78630	3	US-09-949-016-16790
14	323.4	11.2	44019	3	US-09-949-016-14902
15	321.6	11.1	9208	3	US-09-949-016-15567
16	321.2	11.1	786431	3	US-09-751-389-3
17	319.2	11.0	4441	3	US-09-949-016-15325
18	319	11.0	11543	3	US-09-949-016-12071
19	319	11.0	11543	3	US-09-949-016-12673
20	319	11.0	11544	3	US-09-949-016-16172
21	319	11.0	11544	3	US-09-949-016-16173
22	319	11.0	11544	3	US-09-949-016-16174
23	319	11.0	11544	3	US-09-949-016-16175
24	318.2	11.0	37292	3	US-09-949-016-15382

25	318	11.0	40091	3	US-09-949-016-16011	Sequence 16011, A
26	317.2	11.0	26314	3	US-09-949-016-16389	Sequence 16389, A
27	317	11.0	124264	3	US-09-949-016-16396	Sequence 16396, A
c 28	316.8	11.0	53442	3	US-09-949-016-11921	Sequence 11921, A
c 29	316.8	11.0	53453	3	US-09-949-016-13370	Sequence 13370, A
30	316.6	10.9	47347	3	US-09-949-016-14130	Sequence 14130, A
31	316.6	10.9	49721	3	US-09-949-016-17538	Sequence 17538, A
32	316.6	10.9	100463	3	US-09-949-016-12511	Sequence 12511, A
33	316.6	10.9	100468	3	US-09-949-016-13725	Sequence 13725, A
34	315.6	10.9	84252	3	US-09-949-016-17315	Sequence 17315, A
c 35	315.4	10.9	55114	3	US-09-949-016-16792	Sequence 16792, A
c 36	315.4	10.9	116592	3	US-09-818-512-3	Sequence 3, Appli
c 37	315.4	10.9	116592	3	US-10-354-065-3	Sequence 3, Appli
c 38	315.2	10.9	75929	3	US-09-949-016-15543	Sequence 15543, A
c 39	315.2	10.9	75929	3	US-09-949-016-15544	Sequence 15544, A
40	314.6	10.9	1831	3	US-09-949-016-13694	Sequence 13694, A
41	314.4	10.9	23932	3	US-09-949-016-16099	Sequence 16099, A
42	313.8	10.8	25401	3	US-09-949-016-13345	Sequence 13345, A
c 43	313.6	10.8	118143	3	US-09-949-016-17196	Sequence 17196, A
c 44	312.8	10.8	55114	3	US-09-949-016-16792	Sequence 16792, A
c 45	312.4	10.8	49848	3	US-09-949-016-15675	Sequence 15675, A

## ALIGNMENTS

## RESULT 1

US-09-596-141C-3  
; Sequence 3, Application US/09596141C  
; Patent No. 6821774  
; GENERAL INFORMATION:  
; APPLICANT: Lawn, Richard M.  
; APPLICANT: Wade, David  
; APPLICANT: Oram, John F.  
; APPLICANT: Garvin, Michael  
; TITLE OF INVENTION: Compositions and Methods for Increasing Cholesterol  
; TITLE OF INVENTION: Eflux and Raising HDL using ATP Binding Cassette  
; TITLE OF INVENTION: Transporter Protein ABC1  
; FILE REFERENCE: 99,395-B  
; CURRENT APPLICATION NUMBER: US/09/596,141C  
; CURRENT FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: US 60/140,264  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: US 60/153,872  
; PRIOR FILING DATE: 1999-09-14  
; PRIOR APPLICATION NUMBER: US 60/166,573  
; PRIOR FILING DATE: 1999-11-19  
; NUMBER OF SEQ ID NOS: 62  
; SEQ ID NO 3  
; LENGTH: 1643  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-596-141C-3

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Db 16 GGTCCACATGCACTTCCAGGGCTGCTTGGGCTCTTATGCGCTGTGCTGAGTGT 73  
QY 1405 GATAGAACCACTGATGTGAGTACCTGGCTTGGGCTGAGGCTGGAGATCCTGTTGACTG 1464  
Db 74 GATAGAACCACTGATGTGAGTACCTGGGCTTGGGCTGGAGATCCTGTTGACTG 132  
QY 1465 TAGCATGGAGGGCTTGTGAGTCAATGTCTGATGAGGCTGGAGATCCTGGAAT 1524  
Db 133 TAGCATGGAGGGCTTGTGAGTCAATGTCTGATGAGGCTGGAGATCCTGGAAT 191  
QY 1525 ATGATGAGCTGGAGGTGGGAAGAGAGAGTAGGCTTGGGCGAGCTCTCTCATGCCACTCA 1584  
Db 192 ATGATGAGCTGGAGGTGGGAAGAGAGTAGGCTTGGGCGAGCTCTCTCATGCCACTCA 251



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OM nucleic - nucleic search, using sw model

Run on: February 10, 2006, 06:52:37 ; Search time 409,228 Seconds  
(without alignments)  
14034.494 Million cell updates/sec

Title: US-09-846-456A-1

Perfect score: 3231

Sequence: 1 acagggcatgtggcagggtg.....gccccacatccccaccactt 3231

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.\*  
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2: /cgm2\_6/ptodata/1/ina/5 COMB.seq.\*  
3: /cgm2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgm2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgm2\_6/ptodata/1/ina/H COMB.seq.\*  
6: /cgm2\_6/ptodata/1/ina/PCTUS COMB.seq.\*  
7: /cgm2\_6/ptodata/1/ina/PP COMB.seq.\*  
8: /cgm2\_6/ptodata/1/ina/RE COMB.seq.\*  
9: /cgm2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1485.4	46.0	1643	US-09-596-141C-3	Sequence 3, Appli
2	1485.4	46.0	1643	US-09-595-526C-3	Sequence 3, Appli
3	1134.8	35.1	1197	US-09-560-372-1	Sequence 1, Appli
4	347.4	10.8	118143	US-09-949-016-17196	Sequence 13690, A
5	335.6	10.4	13821	US-09-949-016-13690	Sequence 17196, A
6	333	10.3	84870	US-09-949-016-17547	Sequence 17547, A
7	330.4	10.2	36148	US-09-949-016-12969	Sequence 12969, A
8	330	10.2	14519	US-09-949-016-15611	Sequence 15611, A
9	330	10.2	14519	US-09-949-016-15612	Sequence 15612, A
10	325.2	10.1	31318	US-09-949-016-12495	Sequence 12495, A
11	325.2	10.1	31319	US-09-949-016-15963	Sequence 15963, A
12	324.8	10.1	87734	US-09-949-016-17521	Sequence 17521, A
13	324.4	10.0	78630	US-09-949-016-16790	Sequence 16790, A
14	323.4	10.0	44019	US-09-949-016-14902	Sequence 14902, A
15	321.6	10.0	9208	US-09-949-016-15567	Sequence 15567, A
16	321.2	9.9	786431	US-09-751-389-3	Sequence 3, Appli
17	319.2	9.9	4441	US-09-949-016-15325	Sequence 15325, A
18	319	9.9	11543	US-09-949-016-12071	Sequence 12071, A
19	319	9.9	11543	US-09-949-016-12673	Sequence 12673, A
20	319	9.9	11544	US-09-949-016-16172	Sequence 16172, A
21	319	9.9	11544	US-09-949-016-16173	Sequence 16173, A
22	319	9.9	11544	US-09-949-016-16174	Sequence 16174, A
23	319	9.9	11544	US-09-949-016-16175	Sequence 16175, A
24	318.2	9.8	37292	US-09-949-016-15382	Sequence 15382, A

## ALIGNMENTS

### RESULT 1

US-09-596-141C-3  
; Sequence 3, Application US/09596141C  
; Patent No. 6821774  
; GENERAL INFORMATION:  
; APPLICANT: Lawn, Richard M.  
; APPLICANT: Wade, David.  
; APPLICANT: Oram, John P.  
; APPLICANT: Garvin, Michael  
; TITLE OF INVENTION: Compositions and Methods for Increasing Cholesterol  
; TITLE OF INVENTION: Efflux and Raising HDL using ATP Binding Cassette  
; TITLE OF INVENTION: Transporter Protein ABC1  
; FILE REFERENCE: 99.395-B  
; CURRENT APPLICATION NUMBER: US/09/596,141C  
; CURRENT FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: US 60/140,264  
; PRIOR FILING DATE: 1999-06-18  
; PRIOR APPLICATION NUMBER: US 60/153,872  
; PRIOR FILING DATE: 1999-09-14  
; PRIOR APPLICATION NUMBER: US 60/166,573  
; PRIOR FILING DATE: 1999-11-19  
; NUMBER OF SEQ ID NOS: 62  
; SEQ ID NO 3  
; LENGTH: 1643  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-596-141C-3

Query Match 46.0%; Score 1485.4; DB 3; Length 1643;  
Best Local Similarity 98.1%; Pred. No. 0;  
Matches 1615; Conservative 0; Mismatches 6; Indels 26; Gaps 10;

Qy 1345 GCCTCCACATGCACTTCCAGGGCTGCTGGGCTCTTCTATGCGTCTGCTGAGTGT 1404  
Db 16 GGCTCCACATGCACTTCCAGGGCTGCTGGGCTCTTCTATGCGTCTGCTGAGTGT 73  
Qy 1405 GATAGACCACTGATGTGAGTACTGGCTGAGCTGCTGAGCTGCTGAGCTGCTGAGTGT 1464  
Db 74 GATAGACCACTGATGTGAGTACTGGCTGAGCTGCTGAGCTGCTGAGTGT 132  
Qy 1465 TAGCATGAGGGGCTTGTGCGTGAATGTCTGATGCTGCTGAGTGTGGGAGTCTTGGAA 1524  
Db 133 TAGCATGAGGGGCTTGT -CAGCTGAATGTCTGATGCGTGTGGGAGTCTTGGAA 191  
Qy 1525 ATGATGAGCTGGAGTGGGAAGAGAGTAGGCTTGGGGAGCTCTCTCATGCCACCTCA 1584  
Db 192 ATGATGAGCTGGAGTGGGAAGAGAGTAGGCTTGGGGAGCTCTCTCATGCCACCTCA 251